```
     GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTTCTCTGCTCGCCGCTG
   1 ---------+---------+---------+---------+---------+---------+ 60
     CAGGAAGGTGGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAGAGACGAGCGGCGAC
               M  H  S  L  G  F  F  S  V  A  C  S  L  L  A  A  A -

     CGCTGCTCCCGGGTCCTCGCGAGGCGCCCGCCGCCGCCGCCTTCGAGTCCGGACTCG
  61 ---------+---------+---------+---------+---------+---------+ 120
     GCGACGAGGGCCCAGGAGCGCTCCGCGGGCGGCGGCGGCGGAAGCTCAGGCCTGAGC
      L  L  P  G  P  R  E  A  P  A  A  A  A  A  F  E  S  G  L  D -

     ACCTCTCGGACGCGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAAGATCTGG
 121 ---------+---------+---------+---------+---------+---------+ 180
     TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCGTTTCTAGACC
      L  S  D  A  E  P  D  A  G  E  A  T  A  Y  A  S  K  D  L  E -

     AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAAT
 181 ---------+---------+---------+---------+---------+---------+ 240
     TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
      E  Q  L  R  S  V  S  S  V  D  E  L  M  T  V  L  Y  P  E  Y -

     ATTGGAAAATGTACAAGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG
 241 ---------+---------+---------+---------+---------+---------+ 300
     TAACCTTTTACATGTTCACAGTCGATTCCTTTCCTCCGACCGTTGTATTGTCTCTTGTCC
      W  K  M  Y  K  C  Q  L  R  K  G  G  W  Q  H  N  R  E  Q  A -

     CCAACCTCAACTCAAGGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG
```

MATCH WITH FIG. 1B

Fig. 1A

MATCH WITH FIG. 1A

```
301 ---------+---------+---------+---------+---------+---------+ 360
    GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC
     N  L  N  S  R  T  E  E  T  I  K  F  A  A  A  H  Y  N  T  E -

    AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
361 ---------+---------+---------+---------+---------+---------+ 420
    TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
     I  L  K  S  I  D  N  E  W  R  K  T  Q  C  M  P  R  E  V  C -

    GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
421 ---------+---------+---------+---------+---------+---------+ 480
    CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
     I  D  V  G  K  E  F  G  V  A  T  N  T  F  F  K  P  P  C  V -

    TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
481 ---------+---------+---------+---------+---------+---------+ 540
    ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
     S  V  Y  R  C  G  G  C  C  N  S  E  G  L  Q  C  M  N  T  S -

    GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCA
541 ---------+---------+---------+---------+---------+---------+ 600
    CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT
     T  S  Y  L  S  K  T  L  F  E  I  T  V  P  L  S  Q  G  P  K -

    AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
601 ---------+---------+---------+---------+---------+---------+ 660
    TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
     P  V  T  I  S  F  A  N  H  T  S  C  R  C  M  S  K  L  D  V -
```

MATCH WITH FIG. 1C

Fig. 1B

```
                 MATCH WITH FIG. 1B
    TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
661 ---------+---------+---------+---------+---------+---------+ 720
    AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
     Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q -

    AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
721 ---------+---------+---------+---------+---------+---------+ 780
    TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
     A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L -

    TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
781 ---------+---------+---------+---------+---------+---------+ 840
    ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
     A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H -

    ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
841 ---------+---------+---------+---------+---------+---------+ 900
    TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
     D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A -

    CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
901 ---------+---------+---------+---------+---------+---------+ 960
    GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
     G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C -

    GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
961 ---------+---------+---------+---------+---------+---------+ 1020
    CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
                   MATCH WITH FIG. 1D
```

Fig.1C

MATCH WITH FIG. 1C

```
          V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

     ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021 ---------+---------+---------+---------+---------+---------+ 1080
     TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
          T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

     AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081 ---------+---------+---------+---------+---------+---------+ 1140
     TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
          C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

     ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141 ---------+---------+---------+---------+---------+---------+ 1200
     TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
          H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

     CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201 ---------+---------+---------+---------+---------+---------+ 1260
     GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
          G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

     AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

Fig. 1D

MATCH WITH FIG. 1E

MATCH WITH FIG. 1D

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
       M  S  *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 ---------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

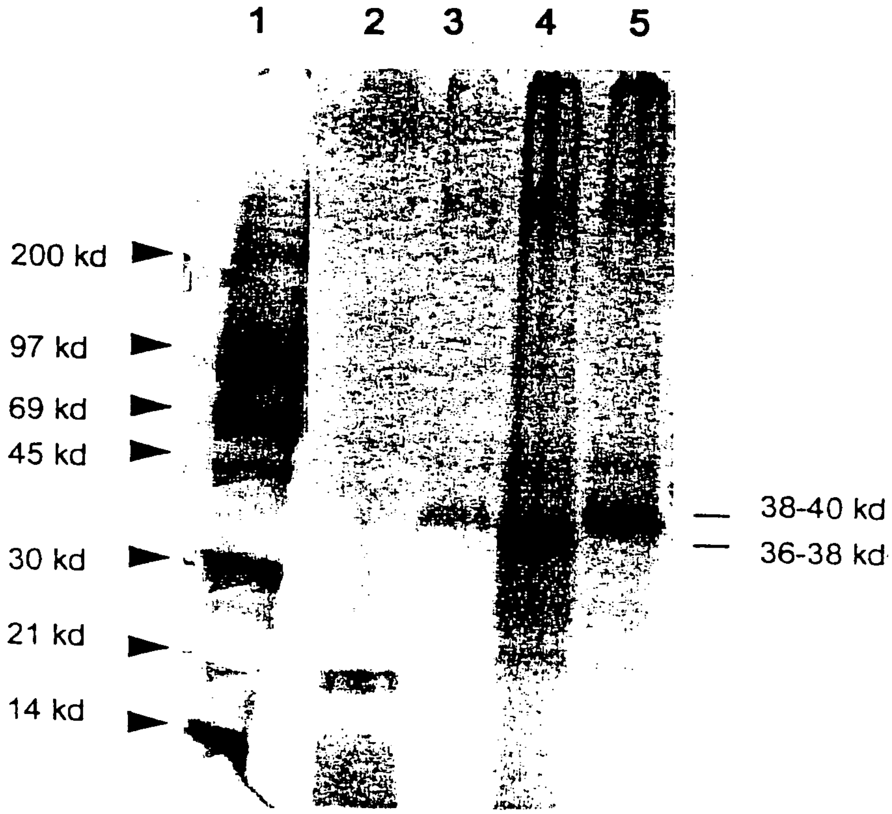
Fig. 1E

```
          1                                                  50
Pdgfa .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf .....MNFLL SWVHWSLALL LY........ .......... .LHHAKWSQA
Vegf2 .......MTV LYPEYWKMYK CQ........ .......... .LRKGGWQHN

      51                                                100
Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... ..........
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... ..........

      101                                               150
Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

      151                                               200
Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT........
Pdgfb QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

Fig. 2A

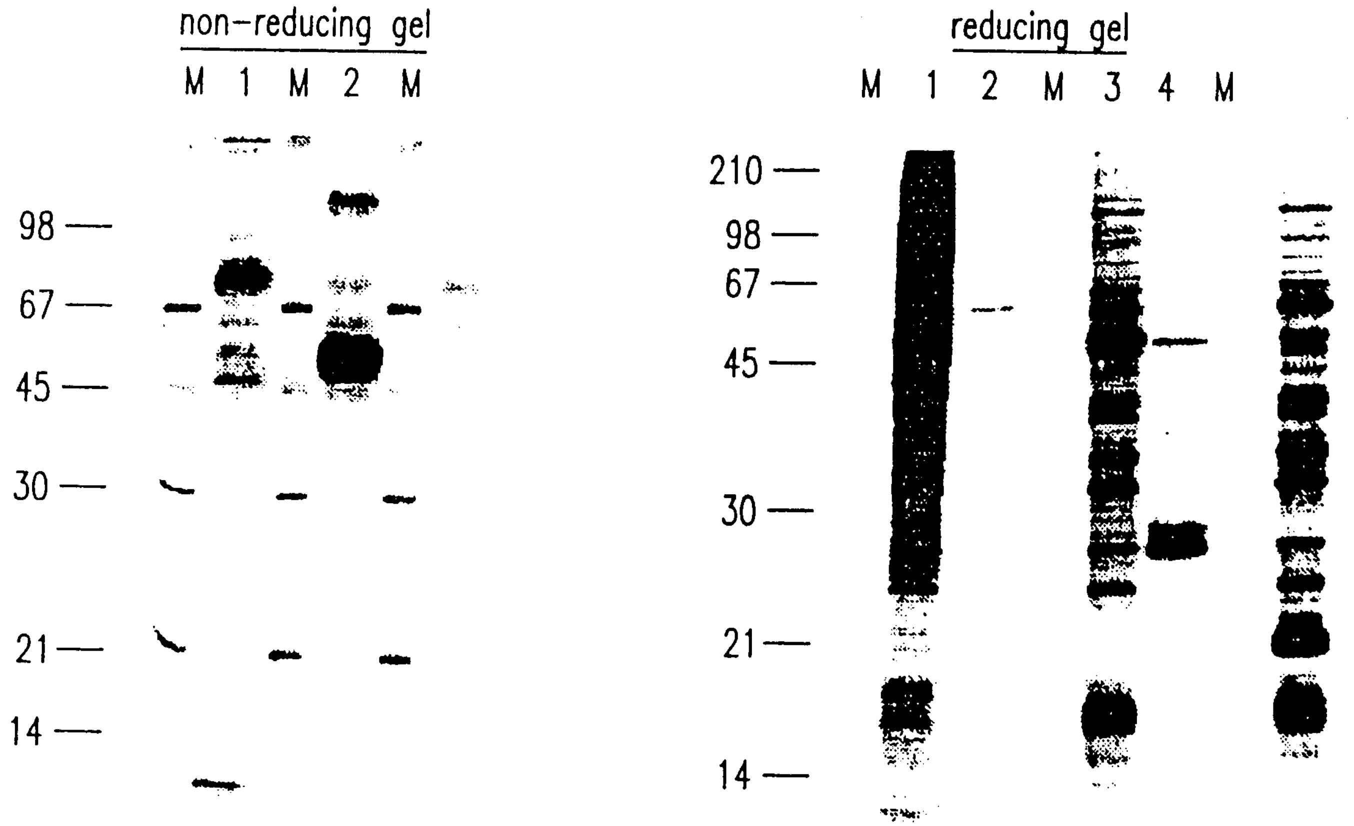
```
       201                                                250
Pdgfa  ....TSLNPD YREEDTDVR. .......... .......... ..........
Pdgfb  RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf  RGK....... .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2  RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

       251                                                300
Pdgfa  .......... .......... .......... .......... ..........
Pdgfb  A......... .......... .......... .......... ..........
 Vegf  ....CGP... .......... .......CSE RRKHLFVQDP QTCKCSCKNT
Vegf2  FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

       301                                                350
Pdgfa  .......... .......... .......... .......... ..........
Pdgfb  .......... .......... .......... .......... ..........
 Vegf  ..DSRCKARQ LELNERTCRC DKPRR..... .......... ..........
Vegf2  LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

       351                                              398
Pdgfa  .......... .......... .......... .......... ........
Pdgfb  .......... .......... .......... .......... ........
 Vegf  .......... .......... .......... .......... ........
Vegf2  KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

Fig. 2B



Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse $ forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

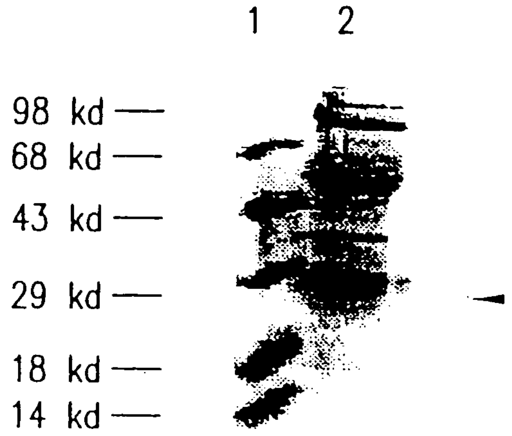
Fig. 3



Lane M Marker
Lane 1 vector medium
Lane 2 VEGF2 medium

Lane M: Marker
Lane 1: vector Cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 Cytoplasm
Lane 4: VEGF2 medium

Fig. 4



Lane 1: Molelular weight marker
Lane 2: Precipitates containing VEGF2.

Fig. 5

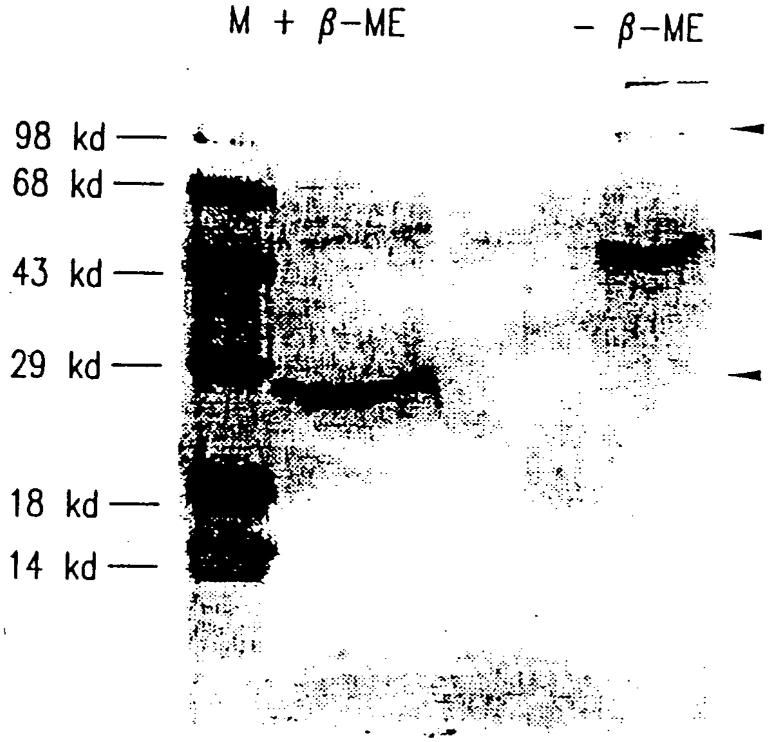


Fig. 6

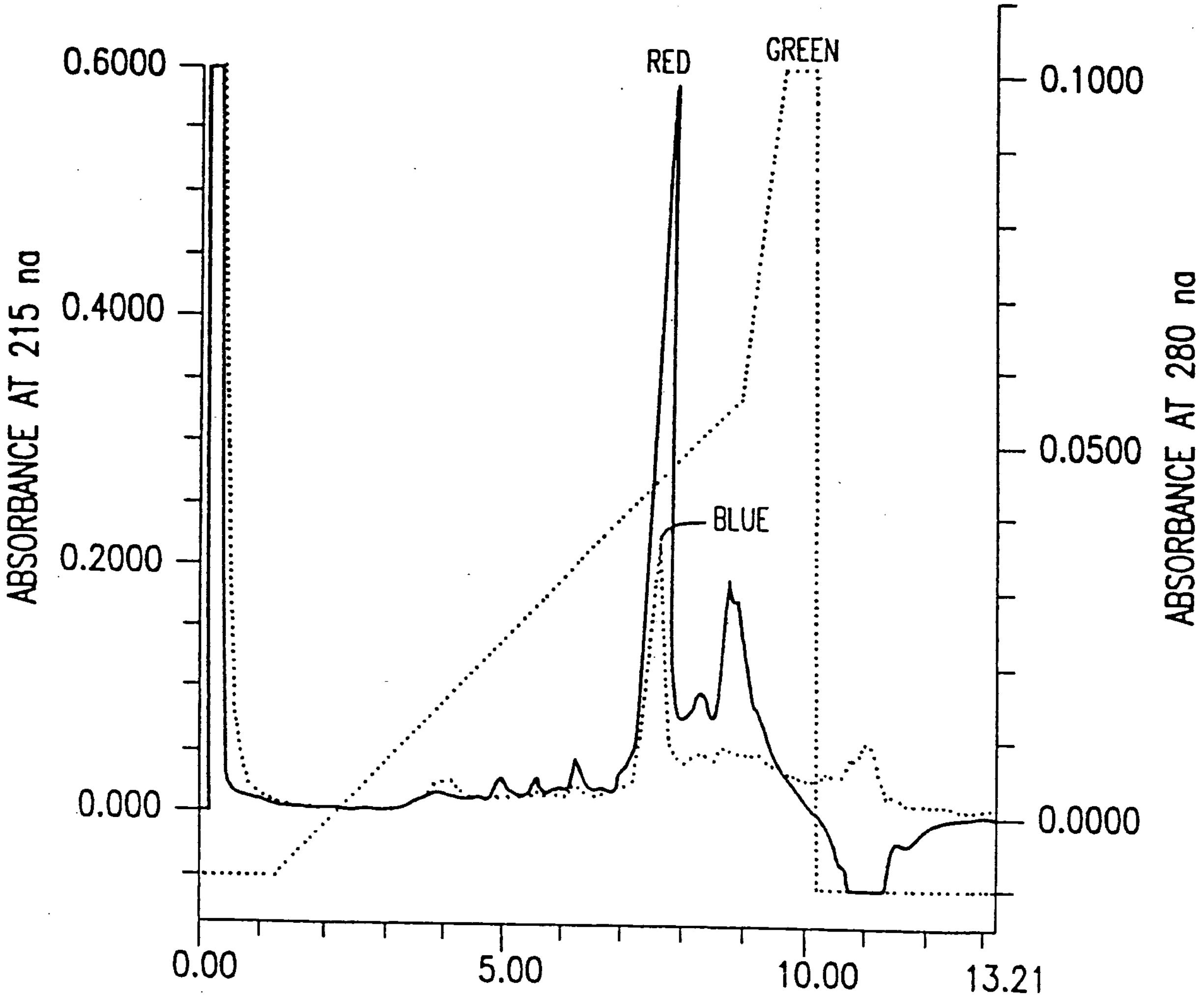

RED
GREEN
BLUE
ABSORBANCE AT 215 na
0.6000
0.4000
0.2000
0.000
ABSORBANCE AT 280 na
0.1000
0.0500
0.0000
0.00
5.00
10.00
13.21

Fig. 7

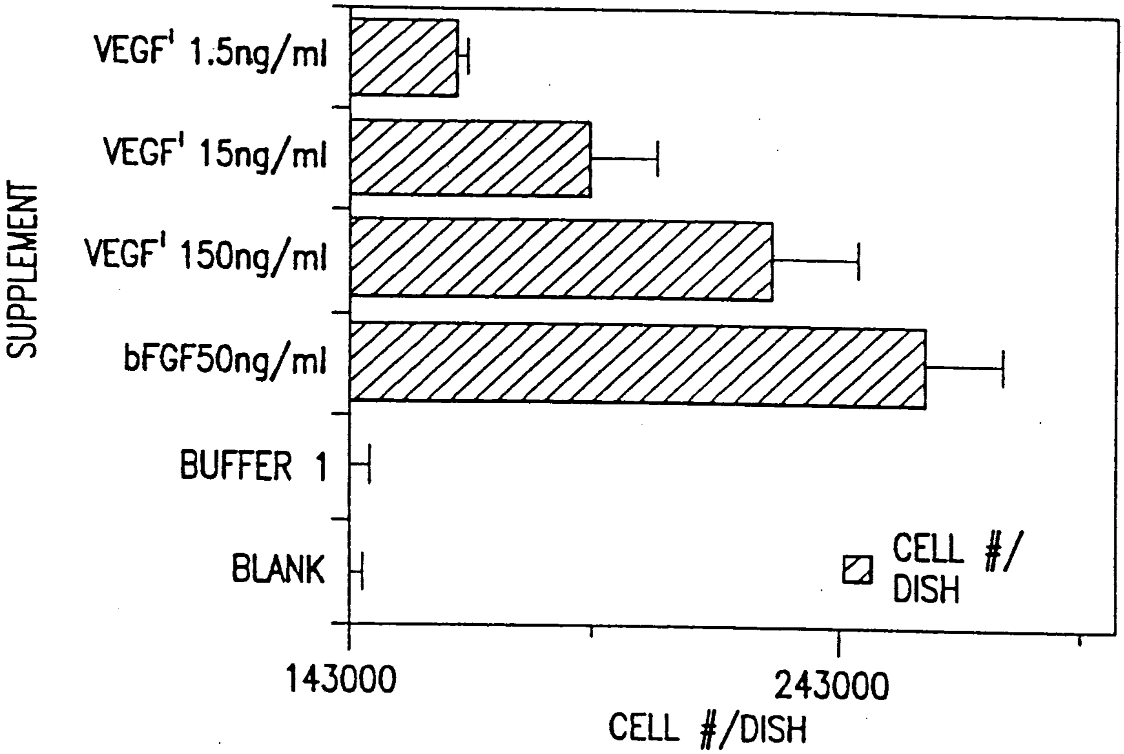

SUPPLEMENT
VEGF' 1.5ng/ml
VEGF' 15ng/ml
VEGF' 150ng/ml
bFGF50ng/ml
BUFFER 1
BLANK
CELL #/ DISH
143000
243000
CELL #/DISH

Fig. 8

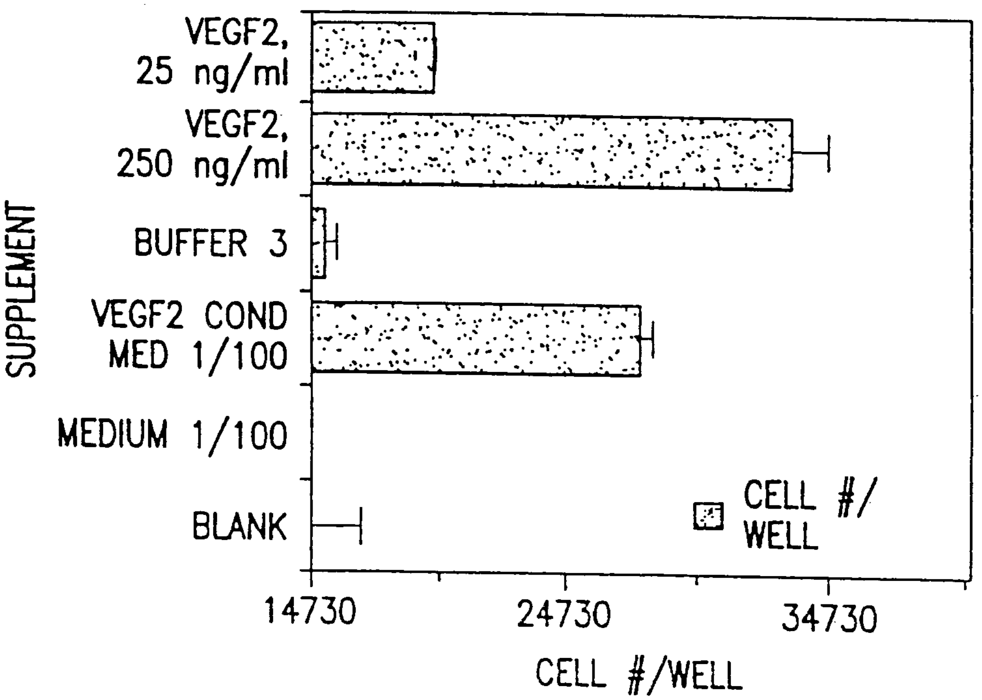

SUPPLEMENT
VEGF2, 25 ng/ml
VEGF2, 250 ng/ml
BUFFER 3
VEGF2 COND MED 1/100
MEDIUM 1/100
BLANK
▨ CELL #/ WELL
14730
24730
34730
CELL #/WELL

Fig. 9